

GenCore version 5.1.6
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Om nucleic - nucleic search, using SW model

Run on: July 23, 2005, 22:27:07 ; Search time 1690 Seconds
(Without alignments)
458.748 Million cell updates/sec

Title: US-09-973-945B-9

Perfect score: 16

Sequence: 1 gaatataatatattc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl;*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_p1:*

9: gb_pr:*

10: gb_ro:*

11: gb_stc:*

12: gb_sy:*

13: gb_un:*

14: gb_vn:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	16	100.0	103	9 HS6A3F	Z55508 H. sapiens C	
2	16	100.0	103	9 HS6A3F	Z55508 H. sapiens C	
3	16	100.0	280	6 CQ70949	CQ70949 Sequence	
4	16	100.0	280	6 CQ70949	CQ70949 Sequence	
5	16	100.0	558	11 G1093	G81093 S208P6414RC	
6	16	100.0	558	11 G1093	G81093 S208P6414RC	
7	16	100.0	559	11 AB165691	AB165691 Bos tauru	
8	16	100.0	559	11 AB165691	AB165691 Bos tauru	
9	16	100.0	566	11 BV0707170	BV0707170 S208P6211	
10	16	100.0	566	11 BV0707170	BV0707170 S208P6211	
11	16	100.0	653	8 IM295790	IM295790 Isoplexis	
12	16	100.0	653	8 IM295790	IM295790 Isoplexis	
13	16	100.0	1022	8 AP518122	AP518122 Templeton	
14	16	100.0	1022	8 AP518122	AP518122 Templeton	
15	16	100.0	1413	5 BC068189	BC068189 Danio rer	
16	16	100.0	1413	5 BC068189	BC068189 Danio rer	
17	16	100.0	4381	9 HS807863	BX647717 Homo sapi	
18	16	100.0	4381	9 HS807863	BX647717 Homo sapi	
19	16	100.0	5728	6 AX345003	AX345003 Sequence	
20	c	21	16	100.0	6059 9 AB023158	AB023158 Homo sapi
21	c	22	16	100.0	6059 9 AB023158	AB023158 Homo sapi
22	c	23	16	100.0	6059 9 AY037299	AY037299 Homo sapi
23	c	24	16	100.0	6059 9 AY037299	AY037299 Homo sapi
24	c	25	16	100.0	6092 6 CQ53660	CQ53660 Sequence
25	c	26	16	100.0	6092 6 CQ53660	CQ53660 Sequence
26	c	27	16	100.0	6792 6 CQ53660	CQ53660 Sequence
27	c	28	16	100.0	6792 6 CQ53660	CQ53660 Sequence
28	c	29	16	100.0	6792 6 CQ53660	CQ53660 Sequence
29	c	30	16	100.0	6792 6 CQ53660	CQ53660 Sequence
30	c	31	16	100.0	7823 6 AX278034	AX278034 Sequence
31	c	32	16	100.0	7823 6 AX278034	AX278034 Sequence
32	c	33	16	100.0	7823 6 AX278034	AX278034 Sequence
33	c	34	16	100.0	7823 6 AX278034	AX278034 Sequence
34	c	35	16	100.0	7823 6 AX278034	AX278034 Sequence
35	c	36	16	100.0	7823 6 AX278034	AX278034 Sequence
36	c	37	16	100.0	8617 3 DMU19731	DMU19731 Drosophila
37	c	38	16	100.0	8617 3 DMU19731	DMU19731 Drosophila
38	c	39	16	100.0	23501 9 AC126176	AC126176 Homo sapi
39	c	40	16	100.0	23501 9 AC126176	AC126176 Homo sapi
40	c	41	16	100.0	23579 6 AX047373	AX047373 Sequence
41	c	42	16	100.0	23579 6 AX047373	AX047373 Sequence
42	c	43	16	100.0	23579 6 CEN1263	CEN1263 Sequence
43	c	44	16	100.0	26246 3 CEN1263	CEN1263 Sequence
44	c	45	16	100.0	26246 3 CEN1263	CEN1263 Sequence
45	c	46	16	100.0	28833 9 AC096581	AC096581 Homo sapi

ALIGNMENTS

RESULT 1
HS46A3F

DEFINITION H. sapiens Cpg island DNA genomic MseI fragment, clone 46a3, forward

ACCESSION 255508

VERSION 255508.1 GI:1021549

KEYWORDS Cpg island; genomic MseI fragment.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1

AUTHORS Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.

TITLE Purification of Cpg islands using a methylated DNA binding column

JOURNAL Nat. Genet. 6 (3), 236-244 (1994)

MEDLINE 9422070

PUBLMED 8012384

REFERENCE 2 (bases 1 to 103)

AUTHORS MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.

TITLE Direct Submission

JOURNAL Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail contact: hungury@sanger.ac.uk

COMMENT Vector: PGM.5ZF(-) Clones are available from the UK MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL: http://www.hgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.

FEATURES Location/Qualifiers

source

1. .103

/organism="Homo Sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="46a3"

/sex="male"

/tissue_type="blood"

/cloneLib="CGI-1"

/dev_STage="adult"

ORIGIN

Query Match 100.0% ; Score 15; DB 9; Length 103;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

OM nucleic - nucleic search, using sw model
 Run on: July 23, 2005, 22:24:32 ; Search time 272 Seconds
 (without alignmentB)
 348.220 Million cell updates/sec

Title: US-09-973-945B-9
Perfect score: 16
Sequence: 1 gatatataataattc 16

Scoring table: IDENTITY NUC
 GapP 10.0 , GapExt 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match: 0%
 Maximum Match: 100%
 Listing first 45 summaries

database :

N_Geneseq_16Feb04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003ab:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004ab:*

13: geneseqn2004bs:*

Result

No.	Score	Query Match Length	DB ID	Description
1	16	100.0	16 6 ABN87616	Abn87616 Native in Abn87616 Native in
2	15	100.0	16 6 ABN87616	Abn87616 Native in Abn87616 Native in
3	16	100.0	16 6 ABN87617	Abn87617 Native in Abn87617 Native in
4	16	100.0	16 6 ABN87617	Abn87617 Native in Abn87617 Native in
5	16	100.0	29 6 ABN87619	Abn87619 Native in Abn87619 Native in
6	16	100.0	29 6 ABN87619	Abn87619 Native in Abn87619 Native in
7	16	100.0	29 6 ABN87618	Abn87618 Native in Abn87618 Native in
8	16	100.0	29 6 ABN87618	Abn87618 Native in Abn87618 Native in
9	16	100.0	46 6 ABN87612	Abn87612 Arabidops Abn87612 Arabidops
10	16	100.0	46 6 ABN87612	Abn87612 Arabidops Abn87612 Arabidops
11	16	100.0	48 6 ARD4422	ARD4422 PCR Prime ARD4422 PCR Prime
12	16	100.0	48 6 ARD4422	ARD4422 PCR Prime ARD4422 PCR Prime
13	16	100.0	58 6 ABN87608	Abn87608 Arabidops Abn87608 Arabidops
14	16	100.0	58 6 ABN87608	Abn87608 Arabidops Abn87608 Arabidops
15	16	100.0	336 4 AAK77535	Aak77535 Human imm Aak77535 Human imm
16	16	100.0	336 4 AAK77535	Aak77535 Human imm Aak77535 Human imm
17	16	100.0	757 4 AAK78539	Aak78539 Human imm Aak78539 Human imm
18	16	100.0	757 4 AAK78539	Aak78539 Human imm Aak78539 Human imm
19	16	100.0	757 4 AAK78540	Aak78540 Human imm Aak78540 Human imm
20	16	100.0	757 4 AAK78540	Aak78540 Human imm Aak78540 Human imm

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1	ABN87616	DE	Native insulator probe NII6 SEQ ID NO:9.
ID	ABNB87616	XX	Arabidopsis thaliana; genetic insulator; gene promoter; plant; transgenic plant; probe; ss.
AC	ABNB87616;	XX	Arabidopsis thaliana.
DT	07-AUG-2002	(first entry)	
XX	XX	DE	Arabidopsis thaliana; genetic insulator; gene promoter; plant; transgenic plant; probe; ss.
XX	XX	XX	Arabidopsis thaliana.
OS	OS	XX	
XX	XX	XX	WO200234035-A1.
PN	PN	XX	11-OCT-2001; 2001WO-US031712.
XX	XX	XX	20-OCT-2000; 2000US-0241735P.
PR	PR	XX	(KENT.) UNIV KENTUCKY RES FOUND.
PA	PA	XX	PI Gan S, Xie M;
XX	XX	XX	DR DR;
PT	PT	XX	New isolated or recombinant polynucleotide cloned from <i>Arabidopsis thaliana</i> , useful for minimizing or eliminating the position effect on a transgene in a plant.
PT	PT	XX	WPI; 2002-471421/50.
PS	PS	XX	Claim 1; Page 21; 45PP; English.
CC	CC	CC	The present invention describes an isolated or a recombinant polynucleotide (I) comprising at least one copy of a polynucleotide having the sequence GATATATATATTC (S1) of 16 nucleotides, or a polynucleotide which is a variant or fragment of S1, where the variant or fragment has a plant genetic insulator activity. Also described are methods: (1) (M1) expressing a polypeptide in a plant cell, involving providing a vector comprising (I), a structural polynucleotide coding for a polypeptide, inserting the vector into a plant cell, where the genetic

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Om nucleic - nucleic search, using sw model

Run on:

July 23, 2005, 22:32:33 ; Search time 402 Seconds

(without alignments)

25.2.508 Million cell updates/sec

Title:

US-09-973-945B-9

Perfect score:

16

Sequence:

1 gaatataatatatttc 16

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

7173243 seqs, 3172128909 residues

Total number of hits satisfying chosen parameters:

14346486

Minimum DB seq length:

0

Maximum DB seq length:

2000000000

Post-processing:

Minimum Match 0%

Listing first 45 summaries

Database:

Published Applications NA: *

1: /cgn2_6/ptodata/2/pupbna/1US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pupbna/1C07_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pupbna/1US06_PUB.seq:*

4: /cgn2_6/ptodata/2/pupbna/1US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pupbna/1US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pupbna/1C07_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pupbna/1US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pupbna/1US09_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pupbna/1US09C_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pupbna/1US09C_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pupbna/1US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pupbna/1US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pupbna/1US10_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pupbna/1US10_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pupbna/1US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pupbna/1US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pupbna/1US10C_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pupbna/1US10C_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pupbna/1US10G_PUBCOMB.seq:*

20: /cgn2_6/ptodata/2/pupbna/1US10H_PUBCOMB.seq:*

21: /cgn2_6/ptodata/2/pupbna/1US10H_PUBCOMB.seq:*

22: /cgn2_6/ptodata/2/pupbna/1US10H_PUBCOMB.seq:*

23: /cgn2_6/ptodata/2/pupbna/1US10H_PUBCOMB.seq:*

24: /cgn2_6/ptodata/2/pupbna/1US11_NEW_PUB.seq:*

25: /cgn2_6/ptodata/2/pupbna/1US60_NEW_PUB.seq:*

26: /cgn2_6/ptodata/2/pupbna/1US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
------------	-------	--------------	-------	-------------

Database:

US-09-973-945A-9

Query Match Similarity 100.0%; Score 16; DB 9; Length 16;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATATATATATTC 16

Db 1 GAATATATATATTC 16

Organism: Arabidopsis thaliana

Software: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 16

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-973-945A-9

RESULT 1
US-09-973-945A-9
; Sequence 9, Application US/09973945A
; Patent No. US2005169397A1
GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: GEN, Susheng
APPLICANT: XIE, Mingtang
TITLE OF INVENTION: Genetic Insulator for Preventing Influence By Another Gene
FILE REFERENCE: 05029-0287
CURRENT APPLICATION NUMBER: US/09/973, 945A
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 6/0741,735
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 16
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-973-945A-9
Query Match Similarity 100.0%; Score 16; DB 9; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATATATATATTC 16
Db 1 GAATATATATATTC 16

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2005, 22:27:43 ; Search time 1838 Seconds

(without alignments)
331.354 Million cell updates/sec

Title: US-09-973-945B-9
Perfect score: 16
Sequence: 1 gaatataatatattc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST*

1: gb_est1:*

2: gb_est2:*

3: gb_hcc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 16 100.0 113 5 BQ173432 BQ173432

2 16 100.0 113 5 BQ173432 BQ173432

3 16 100.0 157 7 CN649902 BQ173432

4 16 100.0 157 7 CN649902 BQ173432

5 16 100.0 188 5 BQ033538 BQ173432

6 16 100.0 188 5 BQ033538 BQ173432

7 16 100.0 202 6 CF01114 BQ173432

8 16 100.0 230 8 AQ927963 BQ173432

9 16 100.0 230 8 AQ927963 BQ173432

10 16 100.0 230 8 AQ927963 BQ173432

11 16 100.0 245 7 CN650739 BQ173432

12 16 100.0 269 2 BF655072 BQ173432

13 16 100.0 269 2 BF655072 BQ173432

14 16 100.0 292 5 BX713976 BQ173432

15 16 100.0 292 5 BX713976 BQ173432

16 16 100.0 303 7 CN650739 BQ173432

17 16 100.0 303 7 CN650739 BQ173432

18 16 100.0 303 7 CN650230 BQ173432

19 16 100.0 303 7 CN650230 BQ173432

20 16 100.0 303 7 CN650230 BQ173432

21 16 100.0 312 8 AQ481031 BQ173432

22 16 100.0 312 8 AQ481031 BQ173432

23 16 100.0 320 4 B1244201 BQ173432

24 16 100.0 320 4 B1244201 BQ173432

ALIGNMENTS

RESULT 1
BQ173432 BQ173432 113 bp mRNA linear EST 18-SEP-2002
DEFINITION BQ173432 mRNA clone Eg_PSGR_03G05 5', mRNA enriched sequence.
ACCESSION BQ173432
VERSION BQ173432.2 GI:23188133
KEYWORDS EST
SOURCE Echinococcus granulosus
ORGANISM Echinococcus granulosus
Cyclophyllidae; Taenidae; Echinococcus.
REFERENCES 1 (bases 1 to 113)
AUTHORS Fernandez, C and Maizels, R.M.
TITLE A survey of genes expressed in Echinococcus granulosus metacestode
JOURNAL Unpublished (2001)
COMMENT On Apr 29, 2002 this sequence version replaced gi:20337834.
Contact: Maizels RM
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, West Mains Road, Edinburgh EH9 3JT, Scotland
Tel: +44 131 650 5511
Fax: +44 131 650 5450
Email: r.maizels@ed.ac.uk
The library was created by Dr Cecilia Fernandez in conjunction with Prof. R. Maizels. Sequencing was also performed by Cecilia. The sequence contained a Polya tail (trimmed).
PCR PRIMERS FORWARD: M13F
BACKWARD: M13R
PLATE: 03 row: G column: 05
Seq. primer: T7
High quality sequence stop: 113.
FEATURES source
1. -113 /organism="Echinococcus granulosus"
/mol_type="mRNA"
/db_xref="taxon:6210"
/clone="Eg_PSGR_03G05"
/dev_stage="larva (protocolex)"
/clone_lib="Echinococcus granulosus protocoolex (full length enriched)"
/note="vector: pSPORT1; Site 1: SalI (5' end); Site 2: NotI (3' end); Echinococcus granulosus is a cestode parasite of dogs (definitive host) and various domestic and wild animals as well as humans (intermediate hosts). The

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GenCore version 5.1.6

OM nucleic - nucleic search, using SW model

Run on: July 23, 2005, 22:28:38 ; search time 99 Seconds
(without alignment)
264.449 Million cell updates/sec

Title: US-09-973-945B-9
perfect score: 16
Sequence: 1 gaatattatataatcc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqb, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/pctodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/pctodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/pctodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/pctodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/pctodata/1/ina/PCITS_COMB.seq: *
6: /cgn2_6/pctodata/1/ina/backfiles1.seq: *

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	16	100.0	48	US-09-545-244A-8
2	16	100.0	48	US-09-545-244A-8
3	16	100.0	37966	US-09-949-016-12566
4	16	100.0	37966	US-09-949-016-12566
5	16	100.0	37966	US-09-949-016-12566
6	16	100.0	9281	US-09-949-016-12182
7	16	100.0	9281	US-09-949-016-12182
8	16	100.0	9281	US-09-949-016-12182
9	16	100.0	251672	US-09-949-016-17296
10	16	100.0	251672	US-09-949-016-17296
11	16	100.0	251682	US-09-949-016-11973
12	16	100.0	251682	US-09-949-016-11973
13	16	100.0	301828	US-09-949-016-13969
14	16	100.0	301828	US-09-949-016-13969
15	15.6	97.5	1974	US-08-413-1353
16	15.6	97.5	1974	US-08-413-1353
17	15.6	97.5	1974	US-08-413-1353
18	15.6	97.5	1974	US-08-413-1353
19	15	93.8	236	US-09-270-767-7457
20	15	93.8	236	US-09-270-767-7457
21	15	93.8	236	US-09-270-767-22739
22	15	93.8	236	US-09-270-767-22739
23	15	93.8	271	US-07-906-871-1
24	15	93.8	271	US-07-906-871-1
25	15	93.8	427	US-09-854-133-551
26	15	93.8	427	US-09-854-133-551
27	15	93.8	488	US-09-270-767-5493

RESULT 1
US-09-545-244A-8

Sequence 8, Application US/09545244A
; Sequence 8, Application US/09545244A
; Patent No. 6388170
; GENERAL INFORMATION:
; APPLICANT: Xie, Mingrui
; APPLICANT: He, Xuehui
; TITLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto
; FILE REFERENCE: 050229-0210
; CURRENT APPLICATION NUMBER: US/09/545, 244A
; CURRENT FILING DATE: 2000-04-07
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Synthetic construct

US-09-545-244A-8

Query Match 100.0%; Score 16; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATATTATATTC 16
Db	9	GAATATTATATTC 24

RESULT 2
US-09-545-244A-8/C
; Sequence 8, Application US/09545244A
; Sequence 8, Application US/09545244A
; Patent No. 6388170
; GENERAL INFORMATION:
; APPLICANT: Gao, Susheng
; APPLICANT: Xie, Mingrui
; APPLICANT: He, Xuehui
; TITLE OF INVENTION: Bidirectional Promoters and Methods Related Thereto
; FILE REFERENCE: 050229-0210
; CURRENT APPLICATION NUMBER: US/09/545, 244A
; CURRENT FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Synthetic construct

US-09-545-244A-8

Query Match 100.0%; Score 16; DB 3; Length 48;